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## RAW SEQUENCE LISTING

DATE: 11/01/2001

PATENT APPLICATION: US/09/821,831

TIME: 10:51:25

Input Set : A:\32061001000.txt

Output Set: N:\CRF3\11012001\I821831.raw

**ENTERED**

4 <110> APPLICANT: Bartlett, Perry Francis  
5 Coulson, Elizabeth Jane  
6 Fieldew, Katrina  
7 Baca, Manuel  
8 Kilpatrick, Trevor  
9 Surindar, Cheema  
11 <120> TITLE OF INVENTION: Method of Modulating Cell Survival and  
12 Reagents Useful for Same  
15 <130> FILE REFERENCE: 3206.1001-000  
17 <140> CURRENT APPLICATION NUMBER: US 09/821,831  
18 <141> CURRENT FILING DATE: 2001-03-30  
20 <150> PRIOR APPLICATION NUMBER: PCT/AU99/00860  
21 <151> PRIOR FILING DATE: 1999-10-05  
23 <150> PRIOR APPLICATION NUMBER: AU PQ0701  
24 <151> PRIOR FILING DATE: 1999-06-01  
26 <150> PRIOR APPLICATION NUMBER: AU PP6351  
27 <151> PRIOR FILING DATE: 1998-10-07  
29 <150> PRIOR APPLICATION NUMBER: AU PP6353  
30 <151> PRIOR FILING DATE: 1998-10-06  
32 <160> NUMBER OF SEQ ID NOS: 72  
34 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
36 <210> SEQ ID NO: 1  
37 <211> LENGTH: 3260  
38 <212> TYPE: DNA  
39 <213> ORGANISM: Artificial Sequence  
41 <220> FEATURE:  
42 <223> OTHER INFORMATION: Synthetic CDNA Sequence of Human  
44 <221> NAME/KEY: CDS  
45 <222> LOCATION: (115)...(1389)  
47 <400> SEQUENCE: 1  
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49 cggctctgcgg agcggactga gctagaagcg gagcgctgac gccggaggcg tgca atg 117  
50 Met  
51 1  
53 agg agg gca ggt gct gcc tgc agc gcc atg gac cgg ctg cgc ctg ctg 165  
54 Arg Arg Ala Gly Ala Ala Cys Ser Ala Met Asp Arg Leu Arg Leu Leu  
55 5 10 15  
57 ctg ctg ctg att cta ggg gtg tcc tct gga ggt gcc aag gag aca tgt 213  
58 Leu Leu Leu Ile Leu Gly Val Ser Ser Gly Gly Ala Lys Glu Thr Cys  
59 20 25 30  
61 tcc aca ggc ctg tac acc cac agc gga gag tgc tgc aaa gcc tgc aac 261  
62 Ser Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn  
63 35 40 45  
65 ttg ggc gaa ggc gtg gcc cag ccc tgc gga gcc aac cag acc gtg tgt 309  
66 Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys  
67 50 55 60 65  
69 gaa ccc tgc ctg gac aat gtt aca ttc tcc gat gtg gtg agc gcc act 357

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70 Glu Pro Cys Leu Asp Asn Val Thr Phe Ser Asp Val Val Ser Ala Thr
71              70              75              80
73 gag ccg tgc aag ccg tgc acc gag tgc ctg ggc ctg cag agc atg tcc 405
74 Glu Pro Cys Lys Pro Cys Thr Glu Cys Leu Gly Leu Gln Ser Met Ser
75              85              90              95
77 gct ccc tgt gtg gag gca gac gat gca gtg tgc aga tgt gcc tat ggc 453
78 Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
79              100              105              110
81 tac tac cag gac gag gag act ggc cac tgt gag gct tgc agc gtg tgc 501
82 Tyr Tyr Gln Asp Glu Glu Thr Gly His Cys Glu Ala Cys Ser Val Cys
83              115              120              125
85 gag gtg ggc tcg gga ctc gtg ttc tcc tgc cag gac aaa cag aac aca 549
86 Glu Val Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
87 130              135              140              145
89 gtg tgt gaa gag tgc cca gag ggc aca tac tca gac gaa gcc aac cac 597
90 Val Cys Glu Glu Cys Pro Glu Gly Thr Tyr Ser Asp Glu Ala Asn His
91              150              155              160
93 gtg gac ccg tgc cta ccc tgc acg gtg tgc gag gac act gag cgc cag 645
94 Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
95              165              170              175
97 tta cgc gag tgc acg ccc tgg gct gat gct gaa tgc gaa gag atc cct 693
98 Leu Arg Glu Cys Thr Pro Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
99              180              185              190
101 ggt cga tgg atc cca agg tct acg ccc ccg gag ggc tcc gac agc aca 741
102 Gly Arg Trp Ile Pro Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
103              195              200              205
105 gcg ccc agc acc cag gag cct gag gtt cct cca gag caa gac ctt gta 789
106 Ala Pro Ser Thr Gln Glu Pro Glu Val Pro Pro Glu Gln Asp Leu Val
107 210              215              220              225
109 ccc agt aca gtg gcg gat atg gtg acc act gtg atg ggc agc tcc cag 837
110 Pro Ser Thr Val Ala Asp Met Val Thr Thr Val Met Gly Ser Ser Gln
111              230              235              240
113 cct gta gtg acc cgc ggc acc acc gac aac ctc att cct gtc tat tgc 885
114 Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys
115              245              250              255
117 tcc atc ttg gct gct gtg gtc gtg ggc ctt gtg gcc tat att gct ttc 933
118 Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe
119              260              265              270
121 aag agg tgg aac agc tgc aaa caa aat aaa caa ggc gcc aac agc cgc 981
122 Lys Arg Trp Asn Ser Cys Lys Gln Asn Lys Gln Gly Ala Asn Ser Arg
123              275              280              285
125 ccc gtg aac cag acg ccc cca ccg gag gga gag aaa ctg cac agc gac 1029
126 Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp
127 290              295              300              305
129 agt ggc atc tct gtg gac agc cag agc ctg cac gac cag cag acc cat 1077
130 Ser Gly Ile Ser Val Asp Ser Gln Ser Leu His Asp Gln Gln Thr His
131              310              315              320
133 acg cag act gcc tca ggc cag gcc ctc aag ggt gat ggc aac ctc tac 1125
134 Thr Gln Thr Ala Ser Gly Gln Ala Leu Lys Gly Asp Gly Asn Leu Tyr

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135          325          330          335
137 agt agc ctg ccc ctg acc aag cgt gag gag gta gag aaa ctg ctc aac 1173
138 Ser Ser Leu Pro Leu Thr Lys Arg Glu Glu Val Glu Lys Leu Leu Asn
139          340          345          350
141 ggg gat acc tgg cga cat ctg gca ggc gag ctg ggt tac cag cct gaa 1221
142 Gly Asp Thr Trp Arg His Leu Ala Gly Glu Leu Gly Tyr Gln Pro Glu
143          355          360          365
145 cat ata gac tcc ttt acc cac gag gcc tgc cca gtg cga gcc ctg ctg 1269
146 His Ile Asp Ser Phe Thr His Glu Ala Cys Pro Val Arg Ala Leu Leu
147 370          375          380          385
149 gcc agc tgg ggt gcc cag gac agt gca acg ctt gat gcc ctt tta gcc 1317
150 Ala Ser Trp Gly Ala Gln Asp Ser Ala Thr Leu Asp Ala Leu Leu Ala
151          390          395          400
153 gcc ctg cga cgc atc cag aga gct gac att gtg gag agt cta tgc agc 1365
154 Ala Leu Arg Arg Ile Gln Arg Ala Asp Ile Val Glu Ser Leu Cys Ser
155          405          410          415
157 gag tcc act gcc aca tcc cca gtg tgaactcaca gactgggagc ccctgtcctg 1419
158 Glu Ser Thr Ala Thr Ser Pro Val
159          420          425
161 tcccacattc cgacgactga tgttctagcc agccccaca gagctgcccc ctctccctcg 1479
162 gggatggccc aacggtcaga acggagcacc tctgtgcagg gcctctgtgt tcccactcct 1539
163 gactccgttg ctgctcccga gggggccctt gcttctgacc accctctcct cagcaagaga 1599
164 gagagagagg accaccogag cctgacttgc tccatttcca tctcaggcct ttccttcctt 1659
165 tctacacatt agctgtgtca gatctggggg tttgacacta ggagaaggga gcggggggcac 1719
166 ccctaagact caggagggtac tgaagaacca gagccatgga ctccacactg tgaaccggag 1779
167 aacaaggggc ggggcattgt ggtaggctag accttcctta gcccctccct tctcccctct 1839
168 ggccaaagaa gaggattacg gacctatctg agctgaaagc aggtttggaa cccagcccac 1899
169 acttctctct cacacacagg atggtaaaac ccagagaaag gcagggactg acctaggcca 1959
170 cccaaccaca ggaagaacaa atgaaggctg atacactccg tttctgaatg agggcgtcaa 2019
171 gtgtgcttgt tgacagggat ggcgtgacct tcagggaagt atctggaagc catgtctgcc 2079
172 ccgccctcaa ccacttccag gccctaccc aaccttgtg cagatgaact gtttgttcaa 2139
173 gggctgggtcc attggtctat tctgatggag tcaagctaag ggctcaggct tatccataag 2199
174 gcatttgttg agagatgaat ctgttagtgc gtcattctt ggcataagcc tgaagccaac 2259
175 acggccctta atgtcagccc tcggggtcag gaaccaagga ctcccacccc acaatccaac 2319
176 actatactac attacacaca cacacacaca cacacacaca cacacacaca cacacacaca 2379
177 gatatcttgc ttttctcccc atggctcttt tggggctgag actagatcct gctgggagtc 2439
178 actgccagtg agagatccgg aggggacaga gctgagcttc atggggctgt cttcctcgcc 2499
179 ccgggtctg gcaggccaag aatgactgca tctgagctgg tgtctgtctt ccaatggcct 2559
180 gtgcgtggag gaaatgctcc cactcctccc cttcttgaag ctgccccag aagactacag 2619
181 tgcaaaagag cagactggtg tgagaacaca agaaaaagca gatgctggcc ctgcagtctg 2679
182 tggcagcttt ctctcagct tcaaggcccc tgcaaaggac ggatttcctg agcacggcca 2739
183 ggaaggggca agagggttcg gttcagtggc gctttctccc ggctccttg cctgttctgt 2799
184 tttgcttgct gttggaatga gtgggcaccc cctctattta gcatgaagga gccccaggca 2859
185 gggatgcac agactgacca ccacccctcc ccacccaggg tccacccaac ccggtgaaga 2919
186 gaccaggagc attgtacgca tacgcgggtg gtatttttat ggaccccaat ctgcaattcc 2979
187 cagacacctg ggaagtggga cattctttgt gtattttat tctccccag gagctgggga 3039
188 gtggtggggg gctgcaggtg cggtttagca tgtgtttgt tctgggggtc tctccagcct 3099
189 tgttttggc caagtggaa cctctggccc tccagctggt gactatgaac tccagacccc 3159
190 ttcgtgctcc ccgacgcctt ccccttgcac cctgtgtaac catttcgttg ggccctccca 3219

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191 aaacctacac ataaaacata caggaggacc attaaattgg c 3260
193 <210> SEQ ID NO: 2
194 <211> LENGTH: 425
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Deduced amino acid sequence
201 <400> SEQUENCE: 2
202 Met Arg Arg Ala Gly Ala Ala Cys Ser Ala Met Asp Arg Leu Arg Leu
203 1 5 10 15
204 Leu Leu Leu Leu Ile Leu Gly Val Ser Ser Gly Gly Ala Lys Glu Thr
205 20 25 30
206 Cys Ser Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys
207 35 40 45
208 Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val
209 50 55 60
210 Cys Glu Pro Cys Leu Asp Asn Val Thr Phe Ser Asp Val Val Ser Ala
211 65 70 75 80
212 Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Leu Gly Leu Gln Ser Met
213 85 90 95
214 Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr
215 100 105 110
216 Gly Tyr Tyr Gln Asp Glu Glu Thr Gly His Cys Glu Ala Cys Ser Val
217 115 120 125
218 Cys Glu Val Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn
219 130 135 140
220 Thr Val Cys Glu Glu Cys Pro Glu Gly Thr Tyr Ser Asp Glu Ala Asn
221 145 150 155 160
222 His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg
223 165 170 175
224 Gln Leu Arg Glu Cys Thr Pro Trp Ala Asp Ala Glu Cys Glu Glu Ile
225 180 185 190
226 Pro Gly Arg Trp Ile Pro Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser
227 195 200 205
228 Thr Ala Pro Ser Thr Gln Glu Pro Glu Val Pro Pro Glu Gln Asp Leu
229 210 215 220
230 Val Pro Ser Thr Val Ala Asp Met Val Thr Thr Val Met Gly Ser Ser
231 225 230 235 240
232 Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr
233 245 250 255
234 Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala
235 260 265 270
236 Phe Lys Arg Trp Asn Ser Cys Lys Gln Asn Lys Gln Gly Ala Asn Ser
237 275 280 285
238 Arg Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser
239 290 295 300
240 Asp Ser Gly Ile Ser Val Asp Ser Gln Ser Leu His Asp Gln Gln Thr
241 305 310 315 320
242 His Thr Gln Thr Ala Ser Gly Gln Ala Leu Lys Gly Asp Gly Asn Leu

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Input Set : A:\32061001000.txt

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243          325          330          335
244 Tyr Ser Ser Leu Pro Leu Thr Lys Arg Glu Glu Val Glu Lys Leu Leu
245          340          345          350
246 Asn Gly Asp Thr Trp Arg His Leu Ala Gly Glu Leu Gly Tyr Gln Pro
247          355          360          365
248 Glu His Ile Asp Ser Phe Thr His Glu Ala Cys Pro Val Arg Ala Leu
249          370          375          380
250 Leu Ala Ser Trp Gly Ala Gln Asp Ser Ala Thr Leu Asp Ala Leu Leu
251 385          390          395          400
252 Ala Ala Leu Arg Arg Ile Gln Arg Ala Asp Ile Val Glu Ser Leu Cys
253          405          410          415
254 Ser Glu Ser Thr Ala Thr Ser Pro Val
255          420          425
258 <210> SEQ ID NO: 3
259 <211> LENGTH: 867
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Synthetic CDNA sequence of rat
266 <221> NAME/KEY: CDS
267 <222> LOCATION: (115)...(867)
269 <400> SEQUENCE: 3
270 acagctccgg cgggcagcag gcgctggagc gcatcgagcgc tcagctcagc gcagcaccat 60
271 cgggtctgcgg agcggactga gctagaagcg gagcgctgac gccggaggcg tgca atg 117
272                                     Met
273                                     1
275 agg agg gca ggt gct gcc tgc agc gcc atg gac cgg ctg cgc ctg ctg 165
276 Arg Arg Ala Gly Ala Ala Cys Ser Ala Met Asp Arg Leu Arg Leu Leu
277          5          10          15
279 ctg ctg ctg att cta ggg gtg tcc tct gga ggt gcc aag gag aca tgt 213
280 Leu Leu Leu Ile Leu Gly Val Ser Ser Gly Gly Ala Lys Glu Thr Cys
281          20          25          30
283 tcc aca ggc ctg tac acc cac agc gga gag tgc tgc aaa gcc tgc aac 261
284 Ser Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
285          35          40          45
287 ttg ggc gaa ggc gtg gcc cag ccc tgc gga gcc aac cag acc gtg tgt 309
288 Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
289 50          55          60          65
291 gaa ccc tgc ctg gac aat gtt aca ttc tcc gat gtg gtg agc gcc act 357
292 Glu Pro Cys Leu Asp Asn Val Thr Phe Ser Asp Val Val Ser Ala Thr
293          70          75          80
295 gag ccg tgc aag ccg tgc acc gag tgc ctg ggc ctg cag agc atg tcc 405
296 Glu Pro Cys Lys Pro Cys Thr Glu Cys Leu Gly Leu Gln Ser Met Ser
297          85          90          95
299 gct ccc tgt gtg gag gca gac gat gca gtg tgc aga tgt gcc tat ggc 453
300 Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
301          100          105          110
303 tac tac cag gac gag gag act ggc cac tgt gag gct tgc agc gtg tgc 501
304 Tyr Tyr Gln Asp Glu Glu Thr Gly His Cys Glu Ala Cys Ser Val Cys

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/821,831

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Input Set : A:\32061001000.txt

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